## SEQUENCE LISTING TOO Rec'd PCT/PTO '2'6 AUG 2005

<110> JACQUET, Alain

<120> HYPOALLERGENIC DER P1 AND DER P3 PROTEINS FROM DERMATOGRAPHOIDES PTERONYSSINUS

<130> VB60107

<140> PCT/EP2004/001850 24-02-2004

<150> GB 0304424.5 26-02-2003

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ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His 35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser 50 55 60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240

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	_	tgg Trp 115	_									_	_			384
		cgg Arg		_	_	_	_		_		_			_		432
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		atc Ile														528
_	_	agg Arg		_		_	_	_			_	_	_			57 <b>è</b>
		aat Asn 195														624
	_	ctg Leu		_	_		_	•		_	_					672
_	_	ctg Leu	_	_					_		_				_	720
		aac Asn														768

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Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gl	ly Ile
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Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Ar 165 170 17	
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Ph 180 185 190	
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Il	le Arg

Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile 215 220 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln 230 235 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly 245 250 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp 265 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile 280 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu 295 <210> 3 <211> 302 <212> PRT <213> Artificial Sequence <220> <223> C4R mutant of ProDer p 1 <400> 3 Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn 10 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe 20 25 30 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser 55 Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu 70 75 Thr Asn Ala Arg Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu 120 125 Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Glu Leu Val Asp 135 Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile 150 155 Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr 165 170

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				_	_	_	gac Asp		_		_			_	_	432
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Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Arg Gly

Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu 115 120

Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp 130 135 140

Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile 155

Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr

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Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro	o Asn Val Asn Lys Ile Arg
195 200	205
Glu Ala Leu Ala Gln Thr His Ser Ala Il	e Ala Val Ile Ile Gly Ile
210 215	220
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp	p Gly Arg Thr Ile Ile Gln
225 230	235 240
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His	s Ala Val Asn Ile Val Gly
245 25	255
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Tr	p Ile Val Arg Asn Ser Trp
260 265	270
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		gcc Ala	_	_					_		_			_	_	288
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		tgg Trp 115														384
		cgg Arg		_	-	_	•		_		_			_	_	432
		tcc Ser														480
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_	_	agg Arg		_		_	_	_			_	_	_			576
		aat Asn 195		_	_						_					624
	_	ctg Leu		_	_		_	_		_	_					672
_	_	ctg Leu	-	-					_		_				_	720
cgc	gac	aac	gga	tat	cag	cca	aac	tac	cac	gcg	gtc	aac	atc	gtg	ggt	768

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Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr 165 170 Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly 180 185 190 Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg 200 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile 215 220 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly 245 250 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp 260 265 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile 280 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu 290 295 300 <210> 8 <211> 909 <212> DNA <213> Artificial Sequence <220> <221> CDS <222> (1) ... (906) <223> C65R mutant of ProDer p 1 <400> 8 cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48 Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn 5 15 aag agc tat gcc acc ttc gag gac gag gcc gcg cgc aag aac ttc 96 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe 20 25 30 ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His 35 40 ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

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Thr	Asn	Ala	Cys	Ser	Ile	Asn	Gly	Asn	Ala	Pro	Ala	Glu	Ile	Asp	Leu	
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Val	Ala	Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn	Ala	Gln	Arg	Phe	Gly	
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GIU	210	neu	Ala	GTII	1111	H1S	ser	Ala	тте	ATG	220	тте	тте	GTĀ	тте	
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145					150					155					160	
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-				•												
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_	_		_				•	• •	•	Ala		_	_			
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_	_	_					_	_		Gly		_				733
neα	GIU	35	val	пур	тут	vaı	40	PET	UDII	GTÄ	GTÀ	45	116	USII	1179	
		33					40					40				
at-	+	~~~	a+~	+ = +	++-	<b>~</b> ~~	~~~	++-	22~	222	~~~	++-	a+~	a+~	200	1021
clg	LCC	yac	cug	LCC	ıta	gac	yag	LCC	aag	aac	cgg	LCC	cug	acg	ayc	192

Leu	Ser 50	Asp	Leu	Ser	Leu	Asp 55	Glu	Phe	Lys	Asn	Arg 60	Phe	Leu	Met	Ser	
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_	_	_			gtg Val				_	_						336
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_	_				gga Gly 150	_			_	_			_			480
_			_		aat Asn		-		-	-	_			_		528
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				_	cag Gln						_		_			624
	•	_		_	acg Thr		_	_		_	_					672
_	_	_	-	_	ttc Phe 230				-		_				_	720

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Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile

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				gaa Glu			_				_					240
_			_	agt Ser 85	_				-		-		_	_	_	288
_	_	_		acc Thr					_	-				_		336
	_		_	ttt Phe				_			_	_	_			384
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taa																909
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Leu	Glu	Ser 35	Val	Lys	Tyr	Val	Gln 40	Ser	Asn	Gly	Gly	Ala 45	Ile	Asn	His	
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Ser	Cys	Trp 115	Ala	Phe	Ser	Gly	Val 120	Ala	Ala	Thr	Glu	Ser 125		Tyr	Leu	

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240

225 230

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Glu Tyr Ile	Gln His Asn	Gly Val Val	Gln Glu Ser	Tyr Tyr Arg	Tyr
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Val Ala Arg	Glu Gln Ser	Cys Arg Arg	Pro Asn Ala	Gln Arg Phe	Gly
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Ile Ser Asn	Tyr Arg Gln	Ile Tyr Pro	Pro Asn Val	Asn Lys Ile	Arg
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	Ala Gln Thr		Ile Ala Val	Ile Ile Gly	Ile
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_	_	Arg His Tyr	Asp Gly Arg	Thr Ile Ile	
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Arg Asp Asn		Pro Asn Tyr	His Ala Val		Gly
	245	77-1 3 M	250	255	Mana
Tyr Ser Asn	260		Trp Ile Val	arg Asn Ser 270	Trp
Aco The Aco		265	Gly Tyr Phe		Tle
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	Met Ile Glu		Tyr Val Val		
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+					06
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шув ser туг	20	Giu Asp Giu 25	Glu Ala Ala	arg Lys Asn 30	riie
	20	25		30	
cta daa add					
	ata aaa tac	ata caa aac	aac aac aaa	act ata aat	cac 144
	gtg aaa tac Val Lvs Tvr			_	
			aac ggc ggg Asn Gly Gly	_	

ctg	tcc	gac	ctg	tct	tta	gac	gag	ttc	aag	aac	cgg	ttc	ctg	atg	agc	192
Leu	Ser	Asp	Leu	Ser	Leu	Asp	Glu	Phe	Lys	Asn	Arg	Phe	Leu	Met	Ser	
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gcc	gag	gct	ttc	gaa	cac	ctt	aag	acc	cag	ttt	gat	ctc	aac	gcg	gag	240
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65					70		-			75	_				80	
acc	aac	acc	tgc	agt	atc	aac	aac	aat	gcc	ccc	gct	gag	att	gat	ctg	288
			Cys	_					-							•
				85					90					95		
cac	cag	atσ	agg	acc	at.a	act	ccc	atc	cac	atσ	caa	aac	aac	tac	aaa	336
_	_	_	Arg						_	_				_		
1119	0111	1100	100		V 4 2		110	105	9		0	0-1	110	0,0	013	
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	_		Ala					_				_	_			301
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as s	tac	atc	cag	cat	22 <b>+</b>	aac	ata	ata	cac	<b>~</b> 22	acc	tat	tac	cas	tac	528
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Giu	ıyı	116	GIII	165	ASII	GIY	vai	vai	170	Giu	Ser	TÄT	IYL	175	IYL	
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vai	міа	Arg	Glu 180	GIII	Ser	Cys	Arg	185	PIO	ASII	на	GIII	190	Pile	GIY	
			100					100					190			
a++	tee	22+	+ - +	cc+	a=~	ata	t = ~	000	cc+	22+	acc	227	22~	ata	200	624
			tat	_	_						_		_			024
ire	ser		Tyr	Arg	GIII	TTE	_	Pro	Pro	ASI	Ala		гÃг	тте	Arg	
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	_	_	gcg	_	_		_	_		_	_					672
Glu		ьeu	Ala	GIN	Tnr		ser	А1а	тте	Ата		тте	тте	GTĀ	тте	
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